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RAW SEQUENCE LISTING

DATE: 07/30/2001

PATENT APPLICATION: US/09/881,736

TIME: 15:53:55

Input Set : A:\0652 2260001 seq list.txt

Output Set: N:\CRF3\07302001\I881736.raw

ENTERED

5 <110> APPLICANT: Glotzer, Michael
6 Jantsch-Plunger, Verena
7 Romano, Alper
8 Mishima, Masanori
9 Kaitna, Susanne
11 <120> TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their
use in
12 screening methods
14 <130> FILE REFERENCE: 0652.2260001/EKS/AES
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/881,736
C--> 17 <141> CURRENT FILING DATE: 2001-06-18
19 <150> PRIOR APPLICATION NUMBER: EP 00 112 880.0
20 <151> PRIOR FILING DATE: 2000-06-19
22 <150> PRIOR APPLICATION NUMBER: EP 01 110 554.1
23 <151> PRIOR FILING DATE: 2001-04-30
25 <150> PRIOR APPLICATION NUMBER: 60/241,231
26 <151> PRIOR FILING DATE: 2000-10-18
28 <150> PRIOR APPLICATION NUMBER: To be determined
29 <151> PRIOR FILING DATE: 2001-06-13
32 <160> NUMBER OF SEQ ID NOS: 6
34 <170> SOFTWARE: PatentIn Ver. 2.1
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 3050
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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44 <221> NAME/KEY: 5'UTR
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47 <220> FEATURE:
48 <221> NAME/KEY: CDS
49 <222> LOCATION: (71)..(1969)
51 <220> FEATURE:
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60 cgtgtgaaag atg gat act atg atg ctg aat gtg cgg aat ctg ttt gag 109
62 Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu
63 1 5 10
65 cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157
67 Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln
68 15 20 25
70 ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205
72 Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln
73 30 35 40 45
75 agg act gac cat gag ctg ggg aaa tac aag gat ctt ttg atg aaa gca 253
77 Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala
78 50 55 60

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80 gag act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat 301
82 Glu Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn
83      65      70      75
85 cag gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc 349
87 Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys
88      80      85      90
90 gaa aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt 397
92 Glu Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys
93      95      100      105
95 gac aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg 445
97 Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu
98      110      115      120      125
100 gct ttt ctc aac aga ggc caa cca tcc agc aat gct ggg aac aaa 493
102 Ala Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys
103      130      135      140
105 aga cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc 541
107 Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser
108      145      150      155
110 ttt gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag 589
112 Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys
113      160      165      170
115 act ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag 637
117 Thr Phe Lys Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln
118      175      180      185
120 ttt gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc 685
122 Phe Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly
123      190      195      200      205
125 tct gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg 733
127 Ser Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val
128      210      215      220
130 act gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag 781
132 Thr Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu
133      225      230      235
135 act gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa 829
137 Thr Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln
138      240      245      250
140 cct tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga 877
142 Pro Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg
143      255      260      265
145 act gag aca gac agt gtg ggc acg cca cag agt aat gga ggg atg cgc 925
147 Thr Glu Thr Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg
148      270      275      280      285
150 ctg cat gac ttt gtt tct aag acg gtt att aaa cct gaa tcc tgt gtt 973
152 Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val
153      290      295      300
155 cca tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga 1021
157 Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg
158      305      310      315
160 gac tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt 1069

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162	Asp	Cys	Arg	Val	Val	Ser	His	Pro	Glu	Cys	Arg	Asp	Arg	Cys	Pro	Leu	
163			320					325					330				
165	ccc	tgc	att	cct	acc	ctg	ata	gga	aca	cct	gtc	aag	att	gga	gag	gga	1117
167	Pro	Cys	Ile	Pro	Thr	Leu	Ile	Gly	Thr	Pro	Val	Lys	Ile	Gly	Glu	Gly	
168			335					340					345				
170	atg	ctg	gca	gac	ttt	gtg	tcc	cağ	act	tct	cca	atg	atc	ccc	tcc	att	1165
172	Met	Leu	Ala	Asp	Phe	Val	Ser	Gln	Thr	Ser	Pro	Met	Ile	Pro	Ser	Ile	
173			350					355					360			365	
175	gtt	gtg	cat	tgt	gta	aat	gag	att	gag	caa	aga	ggg	ctg	act	gag	aca	1213
177	Val	Val	His	Cys	Val	Asn	Glu	Ile	Glu	Gln	Arg	Gly	Leu	Thr	Glu	Thr	
178					370					375					380		
180	ggc	ctg	tat	agg	atc	tct	ggc	tgt	gac	cgc	aca	gta	aaa	gag	ctg	aaa	1261
182	Gly	Leu	Tyr	Arg	Ile	Ser	Gly	Cys	Asp	Arg	Thr	Val	Lys	Glu	Leu	Lys	
183				385						390					395		
185	gag	aaa	ttc	ctc	aga	gtg	aaa	act	gta	ccc	ctc	ctc	agc	aaa	gtg	gat	1309
187	Glu	Lys	Phe	Leu	Arg	Val	Lys	Thr	Val	Pro	Leu	Leu	Ser	Lys	Val	Asp	
188			400					405					410				
190	gat	atc	cat	gct	atc	tgt	agc	ctt	cta	aaa	gac	ttt	ctt	cga	aac	ctc	1357
192	Asp	Ile	His	Ala	Ile	Cys	Ser	Leu	Leu	Lys	Asp	Phe	Leu	Arg	Asn	Leu	
193			415					420					425				
195	aaa	gaa	cct	ctt	ctg	acc	ttt	cgc	ctt	aac	aga	gcc	ttt	atg	gaa	gca	1405
197	Lys	Glu	Pro	Leu	Leu	Thr	Phe	Arg	Leu	Asn	Arg	Ala	Phe	Met	Glu	Ala	
198			430					435				440				445	
200	gca	gaa	atc	aca	gat	gaa	gac	aac	agc	ata	gct	gcc	atg	tac	caa	gct	1453
202	Ala	Glu	Ile	Thr	Asp	Glu	Asp	Asn	Ser	Ile	Ala	Ala	Met	Tyr	Gln	Ala	
203					450					455					460		
205	gtt	ggt	gaa	ctg	ccc	cag	gcc	aac	agg	gac	aca	tta	gct	ttc	ctc	atg	1501
207	Val	Gly	Glu	Leu	Pro	Gln	Ala	Asn	Arg	Asp	Thr	Leu	Ala	Phe	Leu	Met	
208				465					470					475			
210	att	cac	ttg	cag	aga	gtg	gct	cag	agt	cca	cat	act	aaa	atg	gat	gtt	1549
212	Ile	His	Leu	Gln	Arg	Val	Ala	Gln	Ser	Pro	His	Thr	Lys	Met	Asp	Val	
213			480					485						490			
215	gcc	aat	ctg	gct	aaa	gtc	ttt	ggc	cct	aca	ata	gtg	gcc	cat	gct	gtg	1597
217	Ala	Asn	Leu	Ala	Lys	Val	Phe	Gly	Pro	Thr	Ile	Val	Ala	His	Ala	Val	
218			495					500					505				
220	ccc	aat	cca	gac	cca	gtg	aca	atg	tca	cag	gac	atc	aag	cgt	caa	ccc	1645
222	Pro	Asn	Pro	Asp	Pro	Val	Thr	Met	Ser	Gln	Asp	Ile	Lys	Arg	Gln	Pro	
223			510					515					520			525	
225	aag	gtg	gtt	gag	cgc	ctg	ctt	tcc	ttg	cct	ctg	gag	tat	tgg	agt	cag	1693
227	Lys	Val	Val	Glu	Arg	Leu	Leu	Ser	Leu	Pro	Leu	Glu	Tyr	Trp	Ser	Gln	
228				530						535					540		
230	ttc	atg	atg	gtg	gag	caa	gag	aac	att	gac	ccc	cta	cat	gtc	att	gaa	1741
232	Phe	Met	Met	Val	Glu	Gln	Glu	Asn	Ile	Asp	Pro	Leu	His	Val	Ile	Glu	
233				545						550				555			
235	aac	tca	aat	gcc	ttt	tca	aca	cca	cag	aca	cca	gat	att	aaa	gtg	agt	1789
237	Asn	Ser	Asn	Ala	Phe	Ser	Thr	Pro	Gln	Thr	Pro	Asp	Ile	Lys	Val	Ser	
238			560					565					570				
240	tta	ctg	gga	cct	gtg	acc	act	cct	gaa	cat	cag	ctt	ctc	aag	act	cct	1837
242	Leu	Leu	Gly	Pro	Val	Thr	Thr	Pro	Glu	His	Gln	Leu	Leu	Lys	Thr	Pro	

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245 tca tct agt tcc ctg tca cag aga gtc cgt tcc acc ctc acc aag aac 1885
247 Ser Ser Ser Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn
248 590      595      600      605
250 act cct aga ttt ggg agc aaa agc aag tct gcc act aac cta gga cga 1933
252 Thr Pro Arg Phe Gly Ser Lys Ser Lys Ser Ala Thr Asn Leu Gly Arg
253      610      615      620
255 caa ggc aac ttt ttt gct tct cca atg ctc aag tga agtcacatct 1979
257 Gln Gly Asn Phe Phe Ala Ser Pro Met Leu Lys
258      625      630
260 gcctgttact tcccagcatt gactgactat aagaaaggac acatctgtac tctgctctgc 2039
263 agcctcctgt actcattact acttttagca ttctccaggc ttttactcaa gtttaattgt 2099
266 gcatgagggt tttattaaaa ctatatatat ctccccttcc ttctcctcaa gtcacataat 2159
269 atcagcactt tgtgctgggc attggtggga gcttttagat gagacatctt tccaggggta 2219
272 gaagggttag tatggaattg gttgtgattc ttttgggga aggggggttat tgttcctttg 2279
275 gcttaaaagcc aaatgctgct catagaatga tcttctcta gtttcattta gaactgattt 2339
278 ccgtgagaca atgacagaaa ccctacctat ctgataagat tagcttgtct cagggtggga 2399
281 agtgggaggg cagggcaaag aaaggattag accagaggat ttaggatgcc tccttctaag 2459
284 aaccagaagt tctcattccc cattatgaac tgagctataa tatggagctt tcataaaaaat 2519
287 gggatgcatt gaggacagaa ctagtgatgg gagtatgctg agctttgatt tggatgatta 2579
290 ggtctttaat agtggtgagt ggcacaacct tgtaaatgtg aaagtacaac tcgtatttat 2639
293 ctctgatgtg ccgctggctg aactttgggt tcatttgggg tcaaagccag tttttctttt 2699
296 aaaattgaat tcattctgat gcttgcccc cataccccca accttgtcca gtggagccca 2759
299 acttctaaag gtcaatatat catcctttgg catcccaact accaataaag agtaggctat 2819
302 aagggaagat tgtcaatatt ttgtggtaag aaaagctaca gtcatttttt ctttgactt 2879
305 tggatgctga aatttttccc atggaacata gccacatcta gatagatgtg agctttttct 2939
308 tctgttaaaa ttattottaa tgtctgtaaa aacgattttc ttctgtagaa tgtttgactt 2999
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317 <211> LENGTH: 632
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 2
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327      20      25      30
329 Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg Thr Asp
330      35      40      45
332 His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu
333      50      55      60
335 Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp
336      65      70      75      80
338 Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu
339      85      90      95
341 Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys Asp Thr Ser
342      100      105      110
344 Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe Leu
345      115      120      125

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347 Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg Leu Ser
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350 Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys
351      145                      150                      155                      160
353 Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys
354                      165                      170                      175
356 Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp
357                      180                      185                      190
359 Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val
360                      195                      200                      205
362 Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro
363      210                      215                      220
365 Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro
366      225                      230                      235                      240
368 Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn
369                      245                      250                      255
371 Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr Glu Thr
372                      260                      265                      270
374 Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp
375                      275                      280                      285
377 Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys Gly
378      290                      295                      300
380 Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg
381      305                      310                      315                      320
383 Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile
384                      325                      330                      335
386 Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala
387                      340                      345                      350
389 Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His
390                      355                      360                      365
392 Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr
393      370                      375                      380
395 Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe
396      385                      390                      395                      400
398 Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His
399                      405                      410                      415
401 Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro
402                      420                      425                      430
404 Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile
405                      435                      440                      445
407 Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu
408      450                      455                      460
410 Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His Leu
411      465                      470                      475                      480
413 Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val Ala Asn Leu
414                      485                      490                      495
416 Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val Pro Asn Pro
417                      500                      505                      510
419 Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro Lys Val Val

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date